



#8

1

## SEQUENCE LISTING

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<120> NUCLEASE

<130> 068800/0281177

<140> 09/883,249

<141> 2001-06-19

<150> GB 0018120.6

<151> 2000-07-24

<160> 18

<170> PatentIn Ver. 2.1

<210> 1

<211> 294

<212> PRT

<213> Bacillus pumilus

<400> 1

Met Gly Val Glu Gln Glu Trp Ile Lys Asn Ile Thr Asp Met Tyr Gln  
1 5 10 15

Ser Pro Glu Leu Ile Pro Ser His Ala Ser Asn Leu Leu His Gln Leu  
20 25 30

Lys Arg Glu Lys Arg Asn Glu Lys Leu Lys Lys Ala Leu Glu Ile Ile  
35 40 45

Thr Pro Asn Tyr Ile Ser Tyr Ile Ser Ile Leu Leu Asn Asn His Asn  
50 55 60

Met Thr Arg Lys Glu Ile Val Ile Leu Val Asp Ala Leu Asn Glu Tyr  
65 70 75 80

Met Asn Thr Leu Arg His Pro Ser Val Lys Ser Val Phe Ser His Gln  
85 90 95

Ala Asp Phe Tyr Ser Ser Val Leu Pro Glu Phe Phe Asn Leu Leu Phe  
100 105 110

Arg Asn Leu Ile Lys Gly Leu Asn Glu Lys Ile Lys Val Asn Ser Gln  
115 120 125

Lys Asp Ile Ile Ile Asp Cys Ile Phe Asp Pro Tyr Asn Glu Gly Arg  
130 135 140

Val Val Phe Lys Lys Lys Arg Val Asp Val Ala Ile Ile Leu Lys Asn  
145 150 155 160

Lys Phe Val Phe Asn Asn Val Glu Ile Ser Asp Phe Ala Ile Pro Leu  
 165 170 175  
 Val Ala Ile Glu Ile Lys Thr Asn Leu Asp Lys Asn Met Leu Ser Gly  
 180 185 190  
 Ile Glu Gln Ser Val Asp Ser Leu Lys Glu Thr Phe Pro Leu Cys Leu  
 195 200 205  
 Tyr Tyr Cys Ile Thr Glu Leu Ala Asp Phe Ala Ile Glu Lys Gln Asn  
 210 215 220  
 Tyr Ala Ser Thr His Ile Asp Glu Val Phe Ile Leu Arg Lys Gln Lys  
 225 230 235 240  
 Arg Gly Pro Val Arg Arg Gly Thr Pro Leu Glu Val Val His Ala Asp  
 245 250 255  
 Leu Ile Leu Glu Val Val Glu Gln Val Gly Glu His Leu Ser Lys Phe  
 260 265 270  
 Lys Asp Pro Ile Lys Thr Leu Lys Ala Arg Met Thr Glu Gly Tyr Leu  
 275 280 285  
 Ile Lys Gly Lys Gly Lys  
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 Glu Lys Gln Lys Asn Val Lys Glu Lys Tyr Leu Gln Gln Ala Tyr Lys  
 20 25 30  
 His Tyr Leu Tyr Phe Arg Arg Ser Ile Asp Gly Leu Glu Ile Thr Asn  
 35 40 45  
 Asp Glu Ala Ile Phe Lys Leu Thr Gln Ala Ala Asn Asn Tyr Arg Asp  
 50 55 60  
 Asn Val Leu Tyr Leu Phe Glu Ser Arg Pro Asn Ser Gly Gln Glu Ala  
 65 70 75 80  
 Phe Arg Tyr Thr Ile Leu Glu Glu Phe Phe Tyr His Leu Phe Lys Asp  
 85 90 95  
 Leu Val Lys Lys Lys Phe Asn Gln Glu Pro Ser Ser Ile Val Met Gly  
 100 105 110  
 Lys Ala Asn Ser Tyr Val Ser Leu Ser Phe Ser Pro Glu Ser Phe Leu  
 115 120 125

a9  
 ant

Gly Leu Tyr Glu Asn Pro Ile Pro Tyr Ile His Thr Lys Asp Gln Asp  
 130 135 140  
 Phe Val Leu Gly Cys Ala Val Asp Leu Lys Ile Ser Pro Lys Asn Glu  
 145 150 155 160  
 Leu Asn Lys Glu Asn Glu Thr Glu Ile Val Val Pro Val Ile Ala Ile  
 165 170 175  
 Glu Cys Lys Thr Tyr Ile Glu Arg Asn Met Leu Asp Ser Cys Ala Ala  
 180 185 190  
 Thr Ala Ser Arg Leu Lys Ala Ala Met Pro Tyr Cys Leu Tyr Ile Val  
 195 200 205  
 Ala Ser Glu Tyr Met Lys Met Asp Gln Ala Tyr Pro Glu Leu Thr Asp  
 210 215 220  
 Ile Asp Glu Val Phe Ile Leu Cys Lys Ala Ser Val Gly Glu Arg Thr  
 225 230 235 240  
 Ala Leu Lys Lys Lys Gly Leu Pro Pro His Lys Leu Asp Glu Asn Leu  
 245 250 255  
 Met Val Glu Leu Phe His Met Val Glu Arg His Leu Asn Arg Val Trp  
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 Trp Ser Pro Asn Glu Ala Leu Ser Arg Gly Arg Val Ile Gly Arg Pro  
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<212> DNA

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oligonucleotide

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<222> (4)

<223> a, t, c or g

<220>

<221> modified\_base

<222> (8)..(10)

<223> a, t, c or g

<400> 3

cctnagcnnn

10

<210> 4

<211> 12

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<213> Artificial Sequence

9  
a  
cont

<220>  
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12

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<400> 5  
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<210> 6  
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29  
 Cont

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53

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27

<210> 8  
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<220>  
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<400> 8  
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27

<210> 9  
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<220>  
 <223> Description of Artificial Sequence: Illustrative  
 conserved motif

Q9  
 Ant

<220>  
 <221> MOD\_RES  
 <222> (1)  
 <223> Glu or Asp

<220>  
 <221> MOD\_RES  
 <222> (2)..(16)  
 <223> Variable amino acid; this region may encompass 9-15  
 residues according to the specification as filed

<220>  
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 <222> (18)  
 <223> Variable amino acid

<400> 9  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
     1                    5                    10                    15

Glu Xaa Lys

<210> 10  
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<220>  
 <223> Description of Artificial Sequence: Illustrative  
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<220>  
 <221> MOD\_RES  
 <222> (3)..(10)  
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<220>  
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 Ser Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Lys  
     1                    5                    10

<210> 11  
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29

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<220>  
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<400> 11  
Thr Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Lys  
1 5 10

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<210> 12
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<220>  
<223> Description of Artificial Sequence: Primer

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<400> 12
tggttatatt gaccatgc
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<210> 13
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<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Primer

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<400> 13
ttaaataagt tgttatagat a
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<210> 14
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<400> 14  
cctaagctca ctctcaatgg tctgcagagg tcagacacgc ttaggcatg

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a<sup>9</sup>  
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<223> Description of Artificial Sequence: Synthetic  
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cctaagcgtg tctgacctct gcagaccatt gagagtgagc ttagggtac

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<212> DNA

<213> Artificial Sequence

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<223> Description of Combined DNA/RNA Molecule: Primer

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<223> Description of Artificial Sequence: Primer

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cgugucugac cugaaaaaat a

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<210> 17

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Combined DNA/RNA Molecule: Primer

<220>

<223> Description of Artificial Sequence: Primer

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gcucacucuc aauggtggcg g

21

<210> 18

<211> 12

<212> PRT

<213> Artificial Sequence

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conserved motif

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<223> Glu or Asp

<220>

<221> MOD\_RES

<222> (2)..(9)

<223> Variable amino acid

29  
Cmt



<220>

<221> MOD\_RES

<222> (11)

<223> Variable amino acid

<400> 18

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Lys

1

5

10

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